



PATENT

Our Docket: P-IX 4143

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Lockridge and Watkins

Serial No.: 09/748,739

Filed: December 26, 2000

For: BUTYRYLCHOLINESTERASE
VARIANTS AND METHODS
OF USE

Group Art Unit: 1623

Examiner: Not yet Assigned

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Box Missing Parts, Commissioner for Patents, Washington, D.C. 20231, on May 30, 2001.

By Astrid R. Spain
Astrid R. Spain, Reg. No. 47,956

May 30, 2001
Date of Signature

Box Missing Parts
Commissioner for Patents
Washington, D.C. 20231

Sir:

STATEMENT UNDER 37 C.F.R. § 1.821(f) and (g)

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 CFR § 1.821(c) and (e), respectively, are the same.

I hereby state that the submission, filed in accordance with 37 C.F.R. § 1.821(g) herein does not include new matter.

Respectfully submitted,

May 30, 2001

Date

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- 1 -

SEQUENCE LISTING

<110> Lockridge, Oksana
Watkins, Jeffrey D.

<120> Butyrylcholinesterase Variants and
Methods of Use

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Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn
85 90 95
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Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
		260						265					270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Gly	Val
		275					280					285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
	290					295					300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305				310						315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
			325						330					335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
		340						345					350		
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
		355					360					365			
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
	370					375					380				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys
385				390						395					400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala
			405						410					415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu
		420						425					430		
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu
		435					440					445			
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser
	450					455					460				
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro
465				470						475					480
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr
			485						490					495	
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr
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Lys	Leu	Arg													

<210> 5
 <211> 2416
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human Butyrylcholinesterase variant

<221> CDS
 <222> (214)...(1935)

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 gaaatcaata tgcataagcaa agtcacaatc atatgcatca gatttctctt ttggtttctt 180
 ttgctctgca tgcttattgg gaagtcacat act gaa gat gac atc ata att gca 234
 Glu Asp Asp Ile Ile Ile Ala
 1 5
 aca aag aat gga aaa gtc aga ggg atg aac ttg aca gtt ttt ggt ggc 282
 Thr Lys Asn Gly Lys Val Arg Gly Met Asn Leu Thr Val Phe Gly Gly
 10 15 20
 acg gta aca gcc ttt ctt gga att ccc tat gca cag cca cct ctt ggt 330
 Thr Val Thr Ala Phe Leu Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly
 25 30 35
 aga ctt cga ttc aaa aag cca cag tct ctg acc aag tgg tct gat att 378
 Arg Leu Arg Phe Lys Lys Pro Gln Ser Leu Thr Lys Trp Ser Asp Ile
 40 45 50 55
 tgg aat gcc aca aaa tat gca aat tct tgc tgt cag aac ata gat caa 426
 Trp Asn Ala Thr Lys Tyr Ala Asn Ser Cys Cys Gln Asn Ile Asp Gln
 60 65 70
 agt ttt cca ggc ttc cat gga tca gag atg tgg aac cca aac act gac 474
 Ser Phe Pro Gly Phe His Gly Ser Glu Met Trp Asn Pro Asn Thr Asp
 75 80 85
 ctc agt gaa gac tgt tta tat cta aat gta tgg att cca gca cct aaa 522
 Leu Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ile Pro Ala Pro Lys
 90 95 100
 cca aaa aat gcc act gta ttg ata tgg att tat ggt ggt ggt ttt caa 570
 Pro Lys Asn Ala Thr Val Leu Ile Trp Ile Tyr Gly Gly Gly Phe Gln
 105 110 115
 act gga aca tca tct tta cat gtt tat gat ggc aag ttt ctg gct cgg 618
 Thr Gly Thr Ser Ser Leu His Val Tyr Asp Gly Lys Phe Leu Ala Arg
 120 125 130 135
 gtt gaa aga gtt att gta gtg tca atg aac tat agg gtg ggt gcc cta 666

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Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	Asn	Tyr	Arg	Val	Gly	Ala	Leu		
				140					145					150			
gga	ttc	tta	gct	ttg	cca	gga	aat	cct	gag	gct	cca	ggg	aac	atg	ggt	714	
Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	Glu	Ala	Pro	Gly	Asn	Met	Gly		
			155				160					165					
tta	ttt	gat	caa	cag	ttg	gct	ctt	cag	tgg	gtt	caa	aaa	aat	ata	gca	762	
Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	Trp	Val	Gln	Lys	Asn	Ile	Ala		
		170					175				180						
gcc	ttt	ggt	gga	aat	cct	aaa	agt	gta	act	ctc	ttt	gga	gaa	agt	gca	810	
Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	Thr	Leu	Phe	Gly	Glu	Ser	Ala		
	185					190					195						
gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	ctt	tct	cct	gga	agc	cat	tca	858	
Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	Leu	Ser	Pro	Gly	Ser	His	Ser		
200					205				210					215			
ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	gga	tcc	ttt	aat	gct	cct	tgg	906	
Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	Gly	Ser	Phe	Asn	Ala	Pro	Trp		
			220					225				230					
gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	aac	aga	acg	ttg	aac	tta	gct	954	
Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	Asn	Arg	Thr	Leu	Asn	Leu	Ala		
		235					240				245						
aaa	ttg	act	ggt	tcg	tct	aga	gag	aat	gag	act	gaa	ata	atc	aag	tgt	1002	
Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	Glu	Thr	Glu	Ile	Ile	Lys	Cys		
	250					255					260						
ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	ctt	ctg	aat	gaa	gca	ttt	gtt	1050	
Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	Leu	Leu	Asn	Glu	Ala	Phe	Val		
	265					270					275						
gtc	ccc	tat	ggg	act	cag	ttg	tca	gta	aac	ttt	ggt	ccg	acc	gtg	gat	1098	
Val	Pro	Tyr	Gly	Thr	Gln	Leu	Ser	Val	Asn	Phe	Gly	Pro	Thr	Val	Asp		
280					285				290					295			
ggt	gat	ttt	ctc	act	gac	atg	cca	gac	ata	tta	ctt	gaa	ctt	gga	caa	1146	
Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	Ile	Leu	Leu	Glu	Leu	Gly	Gln		
			300					305				310					
ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggt	gtt	aat	aaa	gat	gaa	ggg	aca	1194	
Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	Val	Asn	Lys	Asp	Glu	Gly	Thr		
			315					320				325					
gct	ttt	tta	gtc	tat	ggt	gct	cct	ggc	ttc	agc	aaa	gat	aac	aat	agt	1242	
Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	Phe	Ser	Lys	Asp	Asn	Asn	Ser		
		330					335				340						
atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	ggt	tta	aaa	ata	ttt	ttt	cca	1290	
Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	Gly	Leu	Lys	Ile	Phe	Phe	Pro		

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345					350					355					
gga gtg agt gag ttt gga aag gaa tcc atc ctt ttt cat tac aca gac															1338
Gly Val Ser Glu Phe Gly Lys Glu Ser Ile Leu Phe His Tyr Thr Asp															
360					365					370					375
tgg gta gat gat cag aga cct gaa aac tac cgt gag gcc ttg ggt gat															1386
Trp Val Asp Asp Gln Arg Pro Glu Asn Tyr Arg Glu Ala Leu Gly Asp															
380					385					390					
gtt gtt ggg gat tat aat ttc ata tgc cct gcc ttg gag ttc acc aag															1434
Val Val Gly Asp Tyr Asn Phe Ile Cys Pro Ala Leu Glu Phe Thr Lys															
395					400					405					
aag ttc tca gaa tgg gga aat aat gcc ttt ttc tac tat ttt gaa cac															1482
Lys Phe Ser Glu Trp Gly Asn Asn Ala Phe Phe Tyr Tyr Phe Glu His															
410					415					420					
cga tcc tcc aaa ctt ccg tgg cca gaa tgg atg gga gtg atg cat ggc															1530
Arg Ser Ser Lys Leu Pro Trp Pro Glu Trp Met Gly Val Met His Gly															
425					430					435					
tat gaa att gaa ttt gtc ttt ggt tta cct ctg gaa aga aga gat aat															1578
Tyr Glu Ile Glu Phe Val Phe Gly Leu Pro Leu Glu Arg Arg Asp Asn															
440					445					450					455
tac aca aaa gcc gag gaa att ttg agt aga tcc ata gtg aaa cgg tgg															1626
Tyr Thr Lys Ala Glu Glu Ile Leu Ser Arg Ser Ile Val Lys Arg Trp															
460					465					470					
gca aat ttt gca aaa tat ggg aat cca aat gag act cag aac aat agc															1674
Ala Asn Phe Ala Lys Tyr Gly Asn Pro Asn Glu Thr Gln Asn Asn Ser															
475					480					485					
aca agc tgg cct gtc ttc aaa agc act gaa caa aaa tat cta acc ttg															1722
Thr Ser Trp Pro Val Phe Lys Ser Thr Glu Gln Lys Tyr Leu Thr Leu															
490					495					500					
aat aca gag tca aca aga ata atg acg aaa cta cgt gct caa caa tgt															1770
Asn Thr Glu Ser Thr Arg Ile Met Thr Lys Leu Arg Ala Gln Gln Cys															
505					510					515					
cga ttc tgg aca tca ttt ttt cca aaa gtc ttg gaa atg aca gga aat															1818
Arg Phe Trp Thr Ser Phe Phe Pro Lys Val Leu Glu Met Thr Gly Asn															
520					525					530					535
att gat gaa gca gaa tgg gag tgg aaa gca gga ttc cat cgc tgg aac															1866
Ile Asp Glu Ala Glu Trp Glu Trp Lys Ala Gly Phe His Arg Trp Asn															
540					545					550					
aat tac atg atg gac tgg aaa aat caa ttt aac gat tac act agc aag															1914
Asn Tyr Met Met Asp Trp Lys Asn Gln Phe Asn Asp Tyr Thr Ser Lys															
555					560					565					

attttccttt	agatcaaggc	aaaaatatca	ggagcttttt	tacacaccta	ctaaaaaagt	2025
tattatgtag	ctgaaacaaa	aatgccagaa	ggataatatt	gattcctcac	atctttaact	2085
tagtattttta	cctagcattt	caaaacccaa	atgggotagaa	catgtttaat	taaatttcac	2145
aatataaaagt	tctacagtta	attatgtgca	tattaaaaca	atggcctggg	tcaatttctt	2205
tcttttcctta	ataaaatttaa	gttttttccc	cccaaaatta	tcagtgtctt	gcttttagtc	2265
acgtgtattt	tcattaccac	tcgtaaaaag	gtatcttttt	taaatagaatt	aaatattgaa	2325
acactgtaca	ccatagttta	caatattatg	tttcctaatt	aaaataagaa	ttgaatgtca	2385
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<213> Artificial Sequence

<223> Human Butyrylcholinesterase variant

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Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro
			20					25					30		
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser
		35					40					45			
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
	50					55					60				
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
65				70						75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100					105					110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
		115					120					125			
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145				150						155					160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170					175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
		195					200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Phe	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225				230						235					240

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Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn
      245                      250                      255
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile
      260                      265                      270
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Gln Leu Ser Val
      275                      280                      285
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp
      290                      295                      300
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly
305                      310                      315                      320
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly
      325                      330                      335
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu
      340                      345                      350
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser
      355                      360                      365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn
      370                      375                      380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys
385                      390                      395                      400
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
      405                      410                      415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
      420                      425                      430
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu
      435                      440                      445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
      450                      455                      460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
465                      470                      475                      480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
      485                      490                      495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
      500                      505                      510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
      515                      520                      525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
      530                      535                      540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
545                      550                      555                      560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
      565                      570

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<210> 7

<211> 2416

<212> DNA

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<221> CDS

<222> (214)...(1935)

<400> 7

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gaaatcaata	tgcatagcaa	agtcacaatc	atatgcatca	gattttctct	ttggtttctt	180
ttgctctgca	tgcttattgg	gaagtcacat	act gaa gat	gac atc ata	att gca	234
			Glu Asp Asp	Ile Ile Ile	Ala	
			1	5		
aca aag aat	gga aaa gtc	aga ggg atg	aac ttg aca	ggt ttt ggt	ggc	282
Thr Lys Asn	Gly Lys Val	Arg Gly Met	Asn Leu Thr	Val Phe Gly	Gly	
	10	15	20			
acg gta aca	gcc ttt ctt	gga att ccc	tat gca cag	cca cct ctt	ggg	330
Thr Val Thr	Ala Phe Leu	Gly Ile Pro	Tyr Ala Gln	Pro Pro Leu	Gly	
	25	30	35			
aga ctt cga	ttc aaa aag	cca cag tct	ctg acc aag	tgg tct gat	att	378
Arg Leu Arg	Phe Lys Lys	Pro Gln Ser	Leu Thr Lys	Trp Ser Asp	Ile	
	40	45	50		55	
tgg aat gcc	aca aaa tat	gca aat tct	tgc tgt cag	aac ata gat	caa	426
Trp Asn Ala	Thr Lys Tyr	Ala Asn Ser	Cys Cys Gln	Asn Ile Asp	Gln	
	60	65	70			
agt ttt cca	ggc ttc cat	gga tca gag	atg tgg aac	cca aac act	gac	474
Ser Phe Pro	Gly Phe His	Gly Ser Glu	Met Trp Asn	Pro Asn Thr	Asp	
	75	80	85			
ctc agt gaa	gac tgt tta	tat cta aat	gta tgg att	cca gca cct	aaa	522
Leu Ser Glu	Asp Cys Leu	Tyr Leu Asn	Val Trp Ile	Pro Ala Pro	Lys	
	90	95	100			
cca aaa aat	gcc act gta	ttg ata tgg	att tat ggt	ggt ggt ggt	ttt caa	570
Pro Lys Asn	Ala Thr Val	Leu Ile Trp	Ile Tyr Gly	Gly Gly Gly	Phe Gln	
	105	110	115			
act gga aca	tca tct tta	cat gtt tat	gat ggc aag	ttt ctg gct	cgg	618
Thr Gly Thr	Ser Ser Leu	His Val Tyr	Asp Gly Lys	Phe Leu Ala	Arg	
120	125	130	135			
gtt gaa aga	ggt att gta	gtg tca atg	aac tat agg	gtg ggt gcc	cta	666
Val Glu Arg	Val Ile Val	Val Ser Met	Asn Tyr Arg	Val Gly Ala	Leu	
	140	145	150			
gga ttc tta	gct ttg cca	gga aat cct	gag gct cca	ggg aac atg	ggt	714
Gly Phe Leu	Ala Leu Pro	Gly Asn Pro	Glu Ala Pro	Gly Asn Met	Gly	
	155	160	165			
tta ttt gat	caa cag ttg	gct ctt cag	tgg gtt caa	aaa aat ata	gca	762
Leu Phe Asp	Gln Gln Leu	Ala Leu Gln	Trp Val Gln	Lys Asn Ile	Ala	
	170	175	180			

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185 190 195	
gga gca gct tca gtt agc ctg cat ttg ctt tct cct gga agc cat tca	858
Gly Ala Ala Ser Val Ser Leu His Leu Leu Ser Pro Gly Ser His Ser	
200 205 210 215	
ttg ttc acc aga gcc att ctg caa agt gga tcc ttt aat gct cct tgg	906
Leu Phe Thr Arg Ala Ile Leu Gln Ser Gly Ser Phe Asn Ala Pro Trp	
220 225 230	
gcg gta aca tct ctt tat gaa gct agg aac aga acg ttg aac tta gct	954
Ala Val Thr Ser Leu Tyr Glu Ala Arg Asn Arg Thr Leu Asn Leu Ala	
235 240 245	
aaa ttg act ggt tgc tct aga gag aat gag act gaa ata atc aag tgt	1002
Lys Leu Thr Gly Cys Ser Arg Glu Asn Glu Thr Glu Ile Ile Lys Cys	
250 255 260	
ctt aga aat aaa gat ccc caa gaa att ctt ctg aat gaa gca ttt gtt	1050
Leu Arg Asn Lys Asp Pro Gln Glu Ile Leu Leu Asn Glu Ala Phe Val	
265 270 275	
gtc ccc tat ggg act tcg ttg tca gta aac ttt ggt ccg acc gtg gat	1098
Val Pro Tyr Gly Thr Ser Leu Ser Val Asn Phe Gly Pro Thr Val Asp	
280 285 290 295	
ggt gat ttt ctc act gac atg cca gac ata tta ctt gaa ctt gga caa	1146
Gly Asp Phe Leu Thr Asp Met Pro Asp Ile Leu Leu Glu Leu Gly Gln	
300 305 310	
ttt aaa aaa acc cag att ttg gtg ggt gtt aat aaa gat gaa ggg aca	1194
Phe Lys Lys Thr Gln Ile Leu Val Gly Val Asn Lys Asp Glu Gly Thr	
315 320 325	
gct ttt tta gtc tat ggt gct cct ggc ttc agc aaa gat aac aat agt	1242
Ala Phe Leu Val Tyr Gly Ala Pro Gly Phe Ser Lys Asp Asn Asn Ser	
330 335 340	
atc ata act aga aaa gaa ttt cag gaa ggt tta aaa ata ttt ttt cca	1290
Ile Ile Thr Arg Lys Glu Phe Gln Glu Gly Leu Lys Ile Phe Phe Pro	
345 350 355	
gga gtg agt gag ttt gga aag gaa tcc atc ctt ttt cat tac aca gac	1338
Gly Val Ser Glu Phe Gly Lys Glu Ser Ile Leu Phe His Tyr Thr Asp	
360 365 370 375	
tgg gta gat gat cag aga cct gaa aac tac cgt gag gcc ttg ggt gat	1386
Trp Val Asp Asp Gln Arg Pro Glu Asn Tyr Arg Glu Ala Leu Gly Asp	
380 385 390	

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Val Val Gly Asp Tyr Asn Phe Ile Cys Pro Ala Leu Glu Phe Thr Lys
395 400 405

aag ttc tca gaa tgg gga aat aat gcc ttt ttc tac tat ttt gaa cac 1482
Lys Phe Ser Glu Trp Gly Asn Asn Ala Phe Phe Tyr Tyr Phe Glu His
410 415 420

cga tcc tcc aaa ctt ccg tgg cca gaa tgg atg gga gtg atg cat ggc 1530
Arg Ser Ser Lys Leu Pro Trp Pro Glu Trp Met Gly Val Met His Gly
425 430 435

tat gaa att gaa ttt gtc ttt ggt tta cct ctg gaa aga aga gat aat 1578
Tyr Glu Ile Glu Phe Val Phe Gly Leu Pro Leu Glu Arg Arg Asp Asn
440 445 450 455

tac aca aaa gcc gag gaa att ttg agt aga tcc ata gtg aaa cgg tgg 1626
Tyr Thr Lys Ala Glu Glu Ile Leu Ser Arg Ser Ile Val Lys Arg Trp
460 465 470

gca aat ttt gca aaa tat ggg aat cca aat gag act cag aac aat agc 1674
Ala Asn Phe Ala Lys Tyr Gly Asn Pro Asn Glu Thr Gln Asn Asn Ser
475 480 485

aca agc tgg cct gtc ttc aaa agc act gaa caa aaa tat cta acc ttg 1722
Thr Ser Trp Pro Val Phe Lys Ser Thr Glu Gln Lys Tyr Leu Thr Leu
490 495 500

aat aca gag tca aca aga ata atg acg aaa cta cgt gct caa caa tgt 1770
Asn Thr Glu Ser Thr Arg Ile Met Thr Lys Leu Arg Ala Gln Gln Cys
505 510 515

cga ttc tgg aca tca ttt ttt cca aaa gtc ttg gaa atg aca gga aat 1818
Arg Phe Trp Thr Ser Phe Phe Pro Lys Val Leu Glu Met Thr Gly Asn
520 525 530 535

att gat gaa gca gaa tgg gag tgg aaa gca gga ttc cat cgc tgg aac 1866
Ile Asp Glu Ala Glu Trp Glu Trp Lys Ala Gly Phe His Arg Trp Asn
540 545 550

aat tac atg atg gac tgg aaa aat caa ttt aac gat tac act agc aag 1914
Asn Tyr Met Met Asp Trp Lys Asn Gln Phe Asn Asp Tyr Thr Ser Lys
555 560 565

aaa gaa agt tgt gtg ggt ctc taattaatag atttaccctt tatagaacat 1965
Lys Glu Ser Cys Val Gly Leu
570

atcttccttt agatcaaggc aaaaatatca ggagcttttt tacacaccta ctaaaaaagt 2025
tattatgtag ctgaaacaaa aatgccagaa ggataatatt gattcctcac atctttaact 2085
tagtatttta cctagcattt caaaacccaa atggctagaa catgtttaat taaatttcac 2145
aatataaagt tctacagtta attatgtgca tattaaaaca atggcctggg tcaatttcctt 2205
tctttcctta ataaatttaa gttttttccc cccaaaatta tcagtgtctt gcttttagtc 2265

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			20					25					30		
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser
		35					40					45			
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
	50					55					60				
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
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Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
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Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100					105					110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
		115					120					125			
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145				150						155				160	
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170					175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
	195						200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Phe	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225				230						235				240	
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
				245					250					255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
			260					265					270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Ser	Leu	Ser	Val
		275					280					285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
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Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310						315				320

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Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly
      325                      330                      335
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu
      340                      345                      350
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser
      355                      360                      365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn
      370                      375                      380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys
      385                      390                      395                      400
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
      405                      410                      415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
      420                      425                      430
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu
      435                      440                      445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
      450                      455                      460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
      465                      470                      475                      480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
      485                      490                      495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
      500                      505                      510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
      515                      520                      525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
      530                      535                      540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
      545                      550                      555                      560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
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<210> 9

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

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Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu Met Trp
  1                      5                      10                      15

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<210> 10

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

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<210> 11

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<400> 11

Leu Phe Gly Glu Ser Ala Gly Ala
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<210> 12

<211> 11

<212> PRT

<213> Artificial Sequence

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<223> Human Butyrylcholinesterase variant

<400> 12

Ser Gly Ser Phe Asn Ala Pro Trp Ala Val Thr
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<210> 13

<211> 13

<212> PRT

<213> Artificial Sequence

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<223> Human Butyrylcholinesterase variant

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Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val Asn
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<210> 14

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

TOP SECRET - CONFIDENTIAL

<400> 14
Thr Ala Phe Leu Val Tyr
1 5

<210> 15
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Human Butyrylcholinesterase variant

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<210> 16
<211> 2416
<212> DNA
<213> Homo sapiens

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gaaatcaata tgcataagca agtcacaatc atatgcatca gatttctctt ttggtttctt 180
ttgctctgca tgcttattgg gaagtcacat actgaagatg acatcataat tgcaacaaag 240
aatggaaaag tcagagggat gaacttgaca gtttttggtg gcacggtaac agcctttctt 300
ggaattccct atgcacagcc acctcttggg agacttcgat tcaaaaagcc acagtctctg 360
accaagtggg ctgatatttg gaatgccaca aaatatgcaa attcttgctg tcagaacata 420
gatcaaagtt ttccaggctt ccatggatca gagatgtgga acccaaacac tgacctcagt 480
gaagactggt tatatctaaa tgtatggatt ccagcaccta aaccaaataa tgccactgta 540
ttgatatgga tttatgggtg tggttttcaa actggaacat catctttaca tgtttatgat 600
ggcaagtttc tggctcgggt tgaaagagtt attgtagtgt caatgaacta taggggtggg 660
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gatcaacagt tggctcttca gtgggttcaa aaaaatatag cagcctttgg tggaaatcct 780
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ggtgatgttg ttggggatta taatttcata tgccctgcct tggagttcac caagaagttc 1440
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tggccagaat ggatgggagt gatgcatggc tatgaaattg aatttgtctt tggtttacct 1560
ctggaaagaa gagataatta cacaaaagcc gaggaatttt tgagtagatc catagtgaag 1620
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tggcctgtct tcaaaagcac tgaacaaaaa tatctaacct tgaatacaga gtcaacaaga 1740
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tggaacaatt acatgatgga ctggaaaaat caatttaacg attacactag caagaaagaa 1920
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aaggcaaaaa tatcaggagc ttttttacac acctactaaa aaagttatta tgtagctgaa 2040
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tttaagtttt ttccccccaa aattatcagt gctctgcttt tagtcacgtg tattttcatt 2280
accactcgta aaaaggtatc ttttttaaata gaattaaata ttgaaacact gtacaccata 2340
gtttacaata ttatgtttcc taattaaaaa aagaattgaa tgtcaatatg agatattaaa 2400
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<210> 17
 <211> 574
 <212> PRT
 <213> Homo sapiens

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Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro
          20           25           30
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser
          35           40           45
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser
          50           55           60
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu
 65           70           75           80
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn
          85           90           95
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp
          100          105          110
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr
          115          120          125
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met
          130          135          140
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro
          145          150          155          160
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln
          165          170          175
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val
          180          185          190
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu
          195          200          205
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser
          210          215          220
Gly Ser Phe Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg
          225          230          235          240
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn
          245          250          255
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile

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0946739-060404


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<210> 18
<211> 574
<212> PRT
<213> Homo sapiens
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Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro
20 25 30
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser
35 40 45

Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
50						55					60				
Cys	Cys	Gln	Asn	Ile	Gly	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
65					70					75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100					105					110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
	115						120					125			
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145				150					155						160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
			165					170						175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
		180						185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
	195						200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Phe	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225				230							235				240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
			245					250						255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
	260						265						270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val
	275						280					285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
	290					295					300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310					315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
			325					330						335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345					350		
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
	355						360					365			
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
	370					375					380				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys
385					390					395					400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala
			405					410						415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu
		420						425					430		
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu
	435						440					445			
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser
	450					455					460				
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro

FOI b7D b7C b7E


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<210> 20
<211> 574
<212> PRT
<213> Homo sapiens
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Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro
20 25 30
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser

		35					40					45				
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	
	50					55					60					
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	
65					70					75					80	
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	
				85					90					95		
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	
			100					105					110			
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	
		115					120					125				
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	
	130					135					140					
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	
145				150						155					160	
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	
				165					170					175		
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
			180					185					190			
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	
		195					200					205				
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	
	210					215					220					
Gly	Ser	Phe	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	
225				230						235					240	
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
				245					250					255		
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	
		275					280					285				
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295					300					
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
			325						330					335		
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
	370					375					380					
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
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<210> 22
<211> 574
<212> PRT
<213> Felis catus
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20 25 30

Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Phe
	35					40					45				
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
	50					55					60				
Cys	Tyr	Gln	Asn	Ala	Asp	Gln	Ser	Phe	Pro	Gly	Phe	Pro	Gly	Ser	Glu
65					70					75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Thr	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Met	Ile	Trp
			100					105					110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	Pro	Val	Tyr
		115					120					125			
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145					150					155					160
Glu	Val	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170						175
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Gly	Ser	Val	Ser	Leu	His	Leu
		195					200					205			
Leu	Ser	Pro	Arg	Ser	Gln	Pro	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Ser	Asn	Ala	Pro	Trp	Ala	Val	Met	Ser	Leu	Asp	Glu	Ala	Lys
225					230					235					240
Asn	Arg	Thr	Leu	Thr	Leu	Ala	Lys	Phe	Ile	Gly	Cys	Ser	Lys	Glu	Asn
				245					250					255	
Asp	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
			260					265					270		
Leu	Leu	Asn	Glu	Leu	Leu	Val	Val	Pro	Ser	Asp	Thr	Leu	Leu	Ser	Val
		275					280					285			
Asn	Phe	Gly	Pro	Val	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
	290					295					300				
Thr	Leu	Leu	Gln	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310						315				320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
				325					330					335	
Phe	Ser	Lys	Asp	Asn	Asp	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345					350		
Gly	Leu	Lys	Ile	Tyr	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Arg	Glu	Ala
		355					360					365			
Ile	Leu	Phe	Tyr	Tyr	Val	Asp	Leu	Leu	Asp	Asp	Gln	Arg	Ala	Glu	Lys
		370				375					380				
Tyr	Arg	Glu													

450		455		460
Arg Ser Ile Met Asn Tyr Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro				
465		470		480
Asn Gly Thr Gln Asn Asn Ser Thr Arg Trp Pro Ala Phe Arg Ser Thr				
	485		490	495
Asp Gln Lys Tyr Leu Thr Leu Asn Ala Glu Ser Pro Lys Val Tyr Thr				
	500		505	510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Leu Phe Phe Pro Lys				
	515		520	525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Arg Glu Trp Arg				
	530		535	540
Ala Gly Phe Tyr Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln				
545		550		555
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Ala Gly Leu				560
	565		570	

<210> 23
 <211> 574
 <212> PRT
 <213> Rattus sp.

<400> 23

Glu Glu Asp Val Ile Ile Thr Thr Lys Thr Gly Arg Val Arg Gly Leu				
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Ser Met Pro Ile Leu Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro				
	20	25	30	
Tyr Ala Gln Pro Pro Leu Gly Ser Leu Arg Phe Lys Lys Pro Gln Pro				
	35	40	45	
Leu Asn Lys Trp Pro Asp Val Tyr Asn Ala Thr Lys Tyr Ala Asn Ser				
	50	55	60	
Cys Tyr Gln Asn Ile Asp Gln Ala Phe Pro Gly Phe Gln Gly Ser Glu				
65	70	75	80	
Met Trp Asn Pro Asn Thr Asn Leu Ser Glu Asp Cys Leu Tyr Leu Asn				
	85	90	95	
Val Trp Ile Pro Val Pro Lys Pro Lys Asn Ala Thr Val Met Val Trp				
	100	105	110	
Val Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu Pro Val Tyr				
	115	120	125	
Asp Gly Lys Phe Leu Thr Arg Val Glu Arg Val Ile Val Val Ser Met				
	130	135	140	
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Phe Pro Gly Asn Ser				
145	150	155	160	
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln				
	165	170	175	
Trp Ile Gln Arg Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val				
	180	185	190	
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu				
	195	200	205	
Leu Cys Pro Gln Ser Tyr Pro Leu Phe Thr Arg Ala Ile Leu Glu Ser				
	210	215	220	
Gly Ser Ser Asn Ala Pro Trp Ala Val Lys His Pro Glu Glu Ala Arg				
225	230	235	240	

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Asn	Arg	Thr	Leu	Thr	Leu	Ala	Lys	Phe	Ile	Gly	Cys	Ser	Lys	Glu	Asn		
				245					250					255			
Glu	Lys	Glu	Ile	Ile	Thr	Cys	Leu	Arg	Ser	Lys	Asp	Pro	Gln	Glu	Ile		
			260					265					270				
Leu	Leu	Asn	Glu	Lys	Leu	Val	Leu	Pro	Ser	Asp	Ser	Ile	Arg	Ser	Ile		
		275					280					285					
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	His		
	290					295					300						
Thr	Leu	Leu	Gln	Leu	Gly	Lys	Val	Lys	Thr	Ala	Gln	Ile	Leu	Val	Gly		
305					310					315					320		
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly		
			325					330						335			
Phe	Ser	Lys	Asp	Asn	Asp	Ser	Leu	Ile	Thr	Arg	Arg	Glu	Phe	Gln	Glu		
		340					345						350				
Gly	Leu	Asn	Met	Tyr	Phe	Pro	Gly	Val	Ser	Ser	Leu	Gly	Lys	Glu	Ala		
		355					360					365					
Ile	Leu	Phe	Tyr	Tyr	Val	Asp	Trp	Leu	Gly	Asp	Gln	Thr	Pro	Glu	Val		
	370					375					380						
Tyr	Arg	Glu	Ala	Phe	Asp	Asp	Ile	Ile	Gly	Asp	Tyr	Asn	Ile	Ile	Cys		
385					390					395					400		
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ala	Glu	Leu	Glu	Ile	Asn	Ala		
				405					410					415			
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu		
		420						425					430				
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu		
		435					440					445					
Pro	Leu	Glu	Arg	Arg	Val	Asn	Tyr	Thr	Arg	Ala	Glu	Glu	Ile	Phe	Ser		
	450					455					460						
Arg	Ser	Ile	Met	Lys	Thr	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	His	Pro		
465					470					475					480		
Asn	Gly	Thr	Gln	Gly	Asn	Ser	Thr	Val	Trp	Pro	Val	Phe	Thr	Ser	Thr		
				485					490					495			
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Lys	Ser	Lys	Ile	Asn	Ser		
		500						505					510				
Lys	Leu	Arg	Ala	Pro	Gln	Cys	Gln	Phe	Trp	Arg	Leu	Phe	Phe	Pro	Lys		
		515					520					525					
Val	Leu	Glu	Ile	Thr	Gly	Asp	Ile	Asp	Glu	Arg	Glu	Gln	Glu	Trp	Lys		
	530					535					540						
Ala	Gly	Phe	His	Arg	Trp	Ser	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln		
545					550					555					560		
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Thr	Cys	Thr	Asp	Leu				
				565					570								

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<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> human butyrylcholinesterase variant

<400> 24

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34

[illegible]